



#7

## SEQUENCE LISTING

&lt;110&gt; Smith, John

<120> NOVEL MOLECULES OF THE CARD-RELATED  
PROTEIN FAMILY AND USES THEREOF

&lt;130&gt; 07334-340001

&lt;140&gt; 09/996,617

&lt;141&gt; 2001-11-27

&lt;150&gt; 09/931,071

&lt;151&gt; 2001-08-15

&lt;150&gt; 09/428,252

&lt;151&gt; 1999-10-27

&lt;150&gt; 09/340,620

&lt;151&gt; 1999-06-28

&lt;160&gt; 10

&lt;170&gt; FastSEQ for Windows Version 4.0

&lt;210&gt; 1

&lt;211&gt; 5444

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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&lt;221&gt; CDS

&lt;222&gt; (523)...(4809)

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Glu Ser Leu Cys Ser Thr Trp Pro Trp Lys Asn Glu Asp Phe Asn Gln	
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Asp Pro Leu Val Lys Arg Ser Trp Pro Asp Tyr Val Glu Glu Asn Arg	
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470 475 480	
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Ile	Arg	Ala	Phe	Arg	Leu	Val	Lys	Ser	Asn	Lys	Glu	Leu	Trp	Ala	Leu	
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Cys	Leu	Val	Pro	Trp	Val	Ser	Trp	Leu	Ala	Cys	Thr	Cys	Leu	Met	Gln	
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Gln	Met	Lys	Arg	Lys	Glu	Lys	Leu	Thr	Leu	Thr	Ser	Lys	Thr	Thr	Thr	
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acc	ctc	tgt	cta	cat	tac	ctt	gcc	cag	gct	ctc	caa	gct	cag	cca	ttg	2214
Thr	Leu	Cys	Leu	His	Tyr	Leu	Ala	Gln	Ala	Leu	Gln	Ala	Gln	Pro	Leu	
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gat	ggg	gcc	atc	atc	tcc	acc	ttc	ttg	aag	atg	ggt	att	ctt	caa	gag	2358
Asp	Gly	Ala	Ile	Ile	Ser	Thr	Phe	Leu	Lys	Met	Gly	Ile	Leu	Gln	Glu	
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His	Pro	Ile	Pro	Leu	Ser	Tyr	Ser	Phe	Ile	His	Leu	Cys	Phe	Gln	Glu	
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ctg	tta	agt	gat	gag	ggg	gag	aga	gag	atg	gag	aac	atc	ttt	cac	tgc	2598
Leu	Leu	Ser	Asp	Glu	Gly	Glu	Arg	Glu	Met	Glu	Asn	Ile	Phe	His	Cys	
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Arg	Leu	Ser	Gln	Gly	Arg	Asn	Leu	Met	Gln	Trp	Val	Pro	Ser	Leu	Gln	
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ctg	ctg	ctg	cag	cca	cac	tct	ctg	gag	tcc	ctc	cac	tgc	ttg	tac	gag	2694
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agg cag cac aga tca aca tgg agc ccc acc atg gta gtc ctg ttc agg Arg Gln His Arg Ser Thr Trp Ser Pro Thr Met Val Val Leu Phe Arg 775 780 785			2886
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 Ser Leu Ala Pro Arg Glu Gln Glu Ala Pro Gly Thr Gln Trp Pro Leu  
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 Asp Glu Thr Ser Gly Ile Tyr Tyr Thr Glu Ile Arg Glu Arg Glu Arg  
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 Glu Lys Ser Glu Lys Gly Arg Pro Pro Trp Ala Ala Val Val Gly Thr



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Arg	Pro	Glu	Arg	Leu	Phe	Ile	Leu	Asp	Gly	Val	Asp	Glu	Pro	Gly	
				405				410					415		
Trp	Val	Leu	Gln	Glu	Pro	Ser	Ser	Glu	Leu	Cys	Leu	His	Trp	Ser	Gln
			420					425					430		
Pro	Gln	Pro	Ala	Asp	Ala	Leu	Leu	Gly	Ser	Leu	Leu	Gly	Lys	Thr	Ile
		435					440					445			
Leu	Pro	Glu	Ala	Ser	Phe	Leu	Ile	Thr	Ala	Arg	Thr	Thr	Ala	Leu	Gln
		450					455				460				
Asn	Leu	Ile	Pro	Ser	Leu	Glu	Gln	Ala	Arg	Trp	Val	Glu	Val	Leu	Gly
465					470					475					480
Phe	Ser	Glu	Ser	Ser	Arg	Lys	Glu	Tyr	Phe	Tyr	Arg	Tyr	Phe	Thr	Asp
				485					490					495	
Glu	Arg	Gln	Ala	Ile	Arg	Ala	Phe	Arg	Leu	Val	Lys	Ser	Asn	Lys	Glu
			500					505					510		
Leu	Trp	Ala	Leu	Cys	Leu	Val	Pro	Trp	Val	Ser	Trp	Leu	Ala	Cys	Thr
		515					520					525			
Cys	Leu	Met	Gln	Gln	Met	Lys	Arg	Lys	Glu	Lys	Leu	Thr	Leu	Thr	Ser
		530					535				540				
Lys	Thr	Thr	Thr	Thr	Leu	Cys	Leu	His	Tyr	Leu	Ala	Gln	Ala	Leu	Gln
545					550					555					560
Ala	Gln	Pro	Leu	Gly	Pro	Gln	Leu	Arg	Asp	Leu	Cys	Ser	Leu	Ala	Ala
				565					570					575	
Glu	Gly	Ile	Trp	Gln	Lys	Lys	Thr	Leu	Phe	Ser	Pro	Asp	Asp	Leu	Arg
			580					585					590		
Lys	His	Gly	Leu	Asp	Gly	Ala	Ile	Ile	Ser	Thr	Phe	Leu	Lys	Met	Gly
		595					600					605			
Ile	Leu	Gln	Glu	His	Pro	Ile	Pro	Leu	Ser	Tyr	Ser	Phe	Ile	His	Leu
		610					615				620				
Cys	Phe	Gln	Glu	Phe	Phe	Ala	Ala	Met	Ser	Tyr	Val	Leu	Glu	Asp	Glu
625					630					635					640
Lys	Gly	Arg	Gly	Lys	His	Ser	Asn	Cys	Ile	Ile	Asp	Leu	Glu	Lys	Thr
				645					650					655	
Leu	Glu	Ala	Tyr	Gly	Ile	His	Gly	Leu	Phe	Gly	Ala	Ser	Thr	Thr	Arg
			660					665					670		
Phe	Leu	Leu	Gly	Leu	Leu	Ser	Asp	Glu	Gly	Glu	Arg	Glu	Met	Glu	Asn
		675					680						685		

Ile	Phe	His	Cys	Arg	Leu	Ser	Gln	Gly	Arg	Asn	Leu	Met	Gln	Trp	Val	690	695	700
Pro	Ser	Leu	Gln	Leu	Leu	Leu	Gln	Pro	His	Ser	Leu	Glu	Ser	Leu	His	705	710	715
Cys	Leu	Tyr	Glu	Thr	Arg	Asn	Lys	Thr	Phe	Leu	Thr	Gln	Val	Met	Ala	725	730	735
His	Phe	Glu	Glu	Met	Gly	Met	Cys	Val	Glu	Thr	Asp	Met	Glu	Leu	Leu	740	745	750
Val	Cys	Thr	Phe	Cys	Ile	Lys	Phe	Ser	Arg	His	Val	Lys	Lys	Leu	Gln	755	760	765
Leu	Ile	Glu	Gly	Arg	Gln	His	Arg	Ser	Thr	Trp	Ser	Pro	Thr	Met	Val	770	775	780
Val	Leu	Phe	Arg	Trp	Val	Pro	Val	Thr	Asp	Ala	Tyr	Trp	Gln	Ile	Leu	785	790	795
Phe	Ser	Val	Leu	Lys	Val	Thr	Arg	Asn	Leu	Lys	Glu	Leu	Asp	Leu	Ser	805	810	815
Gly	Asn	Ser	Leu	Ser	His	Ser	Ala	Val	Lys	Ser	Leu	Cys	Lys	Thr	Leu	820	825	830
Arg	Arg	Pro	Arg	Cys	Leu	Leu	Glu	Thr	Leu	Arg	Leu	Ala	Gly	Cys	Gly	835	840	845
Leu	Thr	Ala	Glu	Asp	Cys	Lys	Asp	Leu	Ala	Phe	Gly	Leu	Arg	Ala	Asn	850	855	860
Gln	Thr	Leu	Thr	Glu	Leu	Asp	Leu	Ser	Phe	Asn	Val	Leu	Thr	Asp	Ala	865	870	875
Gly	Ala	Lys	His	Leu	Cys	Gln	Arg	Leu	Arg	Gln	Pro	Ser	Cys	Lys	Leu	885	890	895
Gln	Arg	Leu	Gln	Leu	Val	Ser	Cys	Gly	Leu	Thr	Ser	Asp	Cys	Cys	Gln	900	905	910
Asp	Leu	Ala	Ser	Val	Leu	Ser	Ala	Ser	Pro	Ser	Leu	Lys	Glu	Leu	Asp	915	920	925
Leu	Gln	Gln	Asn	Asn	Leu	Asp	Asp	Val	Gly	Val	Arg	Leu	Leu	Cys	Glu	930	935	940
Gly	Leu	Arg	His	Pro	Ala	Cys	Lys	Leu	Ile	Arg	Leu	Gly	Leu	Asp	Gln	945	950	955
Thr	Thr	Leu	Ser	Asp	Glu	Met	Arg	Gln	Glu	Leu	Arg	Ala	Leu	Glu	Gln	965	970	975
Glu	Lys	Pro	Gln	Leu	Leu	Ile	Phe	Ser	Arg	Arg	Lys	Pro	Ser	Val	Met	980	985	990
Thr	Pro	Thr	Glu	Gly	Leu	Asp	Thr	Gly	Glu	Met	Ser	Asn	Ser	Thr	Ser	995	1000	1005
Ser	Leu	Lys	Arg	Gln	Arg	Leu	Gly	Ser	Glu	Arg	Ala	Ala	Ser	His	Val	1010	1015	1020
Ala	Gln	Ala	Asn	Leu	Lys	Leu	Leu	Asp	Val	Ser	Lys	Ile	Phe	Pro	Ile	1025	1030	1035
Ala	Glu	Ile	Ala	Glu	Glu	Ser	Ser	Pro	Glu	Val	Val	Pro	Val	Glu	Leu	1045	1050	1055
Leu	Cys	Val	Pro	Ser	Pro	Ala	Ser	Gln	Gly	Asp	Leu	His	Thr	Lys	Pro	1060	1065	1070
Leu	Gly	Thr	Asp	Asp	Asp	Phe	Trp	Gly	Pro	Thr	Gly	Pro	Val	Ala	Thr	1075	1080	1085
Glu	Val	Val	Asp	Lys	Glu	Lys	Asn	Leu	Tyr	Arg	Val	His	Phe	Pro	Val	1090	1095	1100
Ala	Gly	Ser	Tyr	Arg	Trp	Pro	Asn	Thr	Gly	Leu	Cys	Phe	Val	Met	Arg	1105	1110	1115
Glu	Ala	Val	Thr	Val	Glu	Ile	Glu	Phe	Cys	Val	Trp	Asp	Gln	Phe	Leu	1125	1130	1135
Gly	Glu	Ile	Asn	Pro	Gln	His	Ser	Trp	Met	Val	Ala	Gly	Pro	Leu	Leu			

	1140		1145		1150
Asp	Ile Lys Ala Glu Pro Gly	Ala Val Glu Ala Val His Leu Pro His			
	1155	1160	1165		
Phe	Val Ala Leu Gln Gly Gly His Val Asp Thr Ser Leu Phe Gln Met				
	1170	1175	1180		
Ala	His Phe Lys Glu Glu Gly Met Leu Leu Glu Lys Pro Ala Arg Val				
1185	1190	1195	1200		
Glu	Leu His His Ile Val Leu Glu Asn Pro Ser Phe Ser Pro Leu Gly				
	1205	1210	1215		
Val	Leu Leu Lys Met Ile His Asn Ala Leu Arg Phe Ile Pro Val Thr				
	1220	1225	1230		
Ser	Val Val Leu Leu Tyr His Arg Val His Pro Glu Glu Val Thr Phe				
	1235	1240	1245		
His	Leu Tyr Leu Ile Pro Ser Asp Cys Ser Ile Arg Lys Glu Leu Glu				
	1250	1255	1260		
Leu	Cys Tyr Arg Ser Pro Gly Glu Asp Gln Leu Phe Ser Glu Phe Tyr				
1265	1270	1275	1280		
Val	Gly His Leu Gly Ser Gly Ile Arg Leu Gln Val Lys Asp Lys Lys				
	1285	1290	1295		
Asp	Glu Thr Leu Val Trp Glu Ala Leu Val Lys Pro Gly Asp Leu Met				
	1300	1305	1310		
Pro	Ala Thr Thr Leu Ile Pro Pro Ala Arg Ile Ala Val Pro Ser Pro				
	1315	1320	1325		
Leu	Asp Ala Pro Gln Leu Leu His Phe Val Asp Gln Tyr Arg Glu Gln				
	1330	1335	1340		
Leu	Ile Ala Arg Val Thr Ser Val Glu Val Val Leu Asp Lys Leu His				
1345	1350	1355	1360		
Gly	Gln Val Leu Ser Gln Glu Gln Tyr Glu Arg Val Leu Ala Glu Asn				
	1365	1370	1375		
Thr	Arg Pro Ser Gln Met Arg Lys Leu Phe Ser Leu Ser Gln Ser Trp				
	1380	1385	1390		
Asp	Arg Lys Cys Lys Asp Gly Leu Tyr Gln Ala Leu Lys Glu Thr His				
	1395	1400	1405		
Pro	His Leu Ile Met Glu Leu Trp Glu Lys Gly Ser Lys Lys Gly Leu				
	1410	1415	1420		
Leu	Pro Leu Ser Ser				
1425					

&lt;210&gt; 3

&lt;211&gt; 5059

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (314)...(1606)

&lt;400&gt; 3

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gtgcaagcat	ctgggccatc	ttcaatggta	aaaaagatac	agtaaagaca	taaataccac	180
atttgacaaa	tggaaaaaaa	ggagtgtcca	gaaaagagta	gcagcagtga	ggaagagctg	240
ccgagacggg	tatacaggga	gctaccctgt	gtttctgaga	ccctttgtga	catctcacat	300
tttttccaag	aag atg aga	cag agg cag	agc cat tat	tgt tcc gtg		349
	Met Met Arg	Gln Arg Gln	Ser His Tyr	Cys Ser Val		

1

5

10

ctg ttc ctg agt gtc aac tat ctg ggg ggg aca ttc cca gga gac att	397
Leu Phe Leu Ser Val Asn Tyr Leu Gly Gly Thr Phe Pro Gly Asp Ile	
15 20 25	
tgc tca gaa gag aat caa ata gtt tcc tct tat gct tct aaa gtc tgt	445
Cys Ser Glu Glu Asn Gln Ile Val Ser Ser Tyr Ala Ser Lys Val Cys	
30 35 40	
ttt gag atc gaa gaa gat tat aaa aat cgt cag ttt ctg ggg cct gaa	493
Phe Glu Ile Glu Glu Asp Tyr Lys Asn Arg Gln Phe Leu Gly Pro Glu	
45 50 55 60	
gga aat gtg gat gtt gag ttg att gat aag agc aca aac aga tac agc	541
Gly Asn Val Asp Val Glu Leu Ile Asp Lys Ser Thr Asn Arg Tyr Ser	
65 70 75	
gtt tgg ttc ccc act gct ggc tgg tat ctg tgg tca gcc aca ggc ctc	589
Val Trp Phe Pro Thr Ala Gly Trp Tyr Leu Trp Ser Ala Thr Gly Leu	
80 85 90	
ggc ttc ctg gta agg gat gag gtc aca gtg acg att gcg ttt ggt tcc	637
Gly Phe Leu Val Arg Asp Glu Val Thr Val Thr Ile Ala Phe Gly Ser	
95 100 105	
tgg agt cag cac ctg gcc ctg gac ctg cag cac cat gaa cag tgg ctg	685
Trp Ser Gln His Leu Ala Leu Asp Leu Gln His His Glu Gln Trp Leu	
110 115 120	
gtg ggc ggc ccc ttg ttt gat gtc act gca gag cca gag gag gct gtc	733
Val Gly Gly Pro Leu Phe Asp Val Thr Ala Glu Pro Glu Glu Ala Val	
125 130 135 140	
gcc gaa atc cac ctc ccc cac ttc atc tcc ctc caa ggt gag gtg gac	781
Ala Glu Ile His Leu Pro His Phe Ile Ser Leu Gln Gly Glu Val Asp	
145 150 155	
gtc tcc tgg ttt ctc gtt gcc cat ttt aag aat gaa ggg atg gtc ctg	829
Val Ser Trp Phe Leu Val Ala His Phe Lys Asn Glu Gly Met Val Leu	
160 165 170	
gag cat cca gcc cgg gtg gag cct ttc tat gct gtc ctg gaa agc ccc	877
Glu His Pro Ala Arg Val Glu Pro Phe Tyr Ala Val Leu Glu Ser Pro	
175 180 185	
agc ttc tct ctg atg ggc atc ctg ctg cgg atc gcc agt ggg act cgc	925
Ser Phe Ser Leu Met Gly Ile Leu Leu Arg Ile Ala Ser Gly Thr Arg	
190 195 200	
ctc tcc atc ccc atc act tcc aac aca ttg atc tat tat cac ccc cac	973
Leu Ser Ile Pro Ile Thr Ser Asn Thr Leu Ile Tyr Tyr His Pro His	
205 210 215 220	
ccc gaa gat att aag ttc cac ttg tac ctt gtc ccc agc gac gcc ttg	1021
Pro Glu Asp Ile Lys Phe His Leu Tyr Leu Val Pro Ser Asp Ala Leu	
225 230 235	
cta aca aag gcg ata gat gat gag gaa gat cgc ttc cat ggt gtg cgc	1069

Leu	Thr	Lys	Ala	Ile	Asp	Asp	Glu	Glu	Asp	Arg	Phe	His	Gly	Val	Arg				
			240					245					250						
ctg	cag	act	tcg	ccc	cca	atg	gaa	ccc	ctg	aac	ttt	ggg	tcc	agt	tat	1117			
Leu	Gln	Thr	Ser	Pro	Pro	Met	Glu	Pro	Leu	Asn	Phe	Gly	Ser	Ser	Tyr				
		255					260				265								
att	gtg	tct	aat	tct	gct	aac	ctg	aaa	gta	atg	ccc	aag	gag	ttg	aaa	1165			
Ile	Val	Ser	Asn	Ser	Ala	Asn	Leu	Lys	Val	Met	Pro	Lys	Glu	Leu	Lys				
	270					275					280								
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Leu	Ser	Tyr	Arg	Ser	Pro	Gly	Glu	Ile	Gln	His	Phe	Ser	Lys	Phe	Tyr				
285					290					295					300				
gct	ggg	cag	atg	aag	gaa	ccc	att	caa	ctt	gag	att	act	gaa	aaa	aga	1261			
Ala	Gly	Gln	Met	Lys	Glu	Pro	Ile	Gln	Leu	Glu	Ile	Thr	Glu	Lys	Arg				
			305						310					315					
cat	ggg	act	ttg	gtg	tgg	gat	act	gag	gtg	aag	cca	gtg	gat	ctc	cag	1309			
His	Gly	Thr	Leu	Val	Trp	Asp	Thr	Glu	Val	Lys	Pro	Val	Asp	Leu	Gln				
		320						325					330						
ctt	gta	gct	gca	tca	gcc	cct	cct	cct	ttc	tca	ggg	gca	gcc	ttt	gtg	1357			
Leu	Val	Ala	Ala	Ser	Ala	Pro	Pro	Pro	Phe	Ser	Gly	Ala	Ala	Phe	Val				
	335					340						345							
aag	gag	aac	cac	cgg	caa	ctc	caa	gcc	agg	atg	ggg	gac	ctg	aaa	ggg	1405			
Lys	Glu	Asn	His	Arg	Gln	Leu	Gln	Ala	Arg	Met	Gly	Asp	Leu	Lys	Gly				
	350				355						360								
gtg	ctc	gat	gat	ctc	cag	gac	aat	gag	gtt	ctt	act	gag	aat	gag	aag	1453			
Val	Leu	Asp	Asp	Leu	Gln	Asp	Asn	Glu	Val	Leu	Thr	Glu	Asn	Glu	Lys				
365					370					375					380				
gag	ctg	gtg	gag	cag	gaa	aag	aca	cgg	cag	agc	aag	aat	gag	gcc	ttg	1501			
Glu	Leu	Val	Glu	Gln	Glu	Lys	Thr	Arg	Gln	Ser	Lys	Asn	Glu	Ala	Leu				
			385					390						395					
ctg	agc	atg	gtg	gag	aag	aaa	ggg	gac	ctg	gcc	ctg	gac	gtg	ctc	ttc	1549			
Leu	Ser	Met	Val	Glu	Lys	Lys	Gly	Asp	Leu	Ala	Leu	Asp	Val	Leu	Phe				
		400					405					410							
aga	agc	att	agt	gaa	agg	gac	cct	tac	ctc	gtg	tcc	tat	ctt	aga	cag	1597			
Arg	Ser	Ile	Ser	Glu	Arg	Asp	Pro	Tyr	Leu	Val	Ser	Tyr	Leu	Arg	Gln				
		415				420						425							
cag	aat	ttg	taaaatgagt cagttaggta gtctggaaga gagaatccag													1646			
Gln	Asn	Leu																	
	430																		
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&lt;210&gt; 4

&lt;211&gt; 431

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 4

Met	Met	Arg	Gln	Arg	Gln	Ser	His	Tyr	Cys	Ser	Val	Leu	Phe	Leu	Ser
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			20					25					30		
Asn	Gln	Ile	Val	Ser	Ser	Tyr	Ala	Ser	Lys	Val	Cys	Phe	Glu	Ile	Glu
		35					40					45			
Glu	Asp	Tyr	Lys	Asn	Arg	Gln	Phe	Leu	Gly	Pro	Glu	Gly	Asn	Val	Asp
	50					55					60				
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&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 6

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&lt;211&gt; 740

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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&lt;211&gt; 195

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 8

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&lt;210&gt; 9

&lt;211&gt; 585

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 9

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&lt;210&gt; 10

&lt;211&gt; 740

&lt;212&gt; DNA

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